

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 97	22699

08/836455

PCT/US96/20757

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M G T P A Q I L G F
ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC

L L L L F P G T R C
TTG TTG CTC TTG TTT CCA GGT ACC AGA TGT
(leader, -20-1)

D I Q M T Q S P S S
GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC

L S A S L G Q R V S
TTA TCT GCC TCT CTG GGA CAA AGA GTC AGT

L T C
CTC ACT TGT (fr. 1, 1-23)

R A S Q D I G I N L
CGG GCA AGT CAG GAC ATT GGT ATT AAC TTA

H
CAT (cdr1, 24-34)

T L Q Q E P D G T I
TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT

K R L I Y
AAA CGC CTG ATC TAC (fr2., 35-49)

A T S S L G S
GCC ACA TCC AGT TTA GGT TCT (cdr2, 50-56)

G V P K R F S G S R
GGT GTC CCC AAA AGG TTC AGT GGC AGT AGG

S G S D Y S L T I S
TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC

S L E S G D F V A Y
AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT

Y C
TAC TGT (fr3, 57-88)

L Q Y A S S P Y T
CTA CAA TAT GCT AGT TCT CCG TAC ACG
(cdr3, 89-97)

F G G G T K L E I K
TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA
(fr4, 98-107)

R A D A A P T V S I
CGG GCT GAT GCT GCA CCA ACT GTA TCC ATC

F P P S S K L G
TTC CCA CCA TCC AGT AAG CTT GGG

FIG. 1

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APPROVED	O.G. FIG.	
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DRAFTSMAN	WO 91/22699	

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M E C S W V F L F L L S I T T G V
 ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT GTC
 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly Val

H S
 CAC TCC
 His Ser (leader)

Q A Y L Q Q S G A E L V R S
 CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG TCT
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser

G A S V K M S C K A S G Y T L T
 GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG ACC
 Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr
 (1-30, Fr. #1)

S Y N M H
 AGT TAC AAT ATG CAC
 Ser Tyr Asn Met His (31-35, CDR 1)

W V K Q T P G Q G L E W I G
 TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG GAA TGG ATT GGA
 Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly
 (36-49, Fr. #2)

N I F P G N G D T Y Y N Q K F K G
 AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT CAG AAG TTT AAG GGC
 Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn Gln Lys Phe Lys Gly
 (50-66, CDR 2)

K A S L T A D T S S S T A Y M Q
 AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC ACA GCC TAC ATG CAG
 Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln

I S S L T S E D S A V Y F C A R
 ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC TAT TTC TGT GCA AGA
 Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 (67-98, Fr. #3)

G N W E G A L D Y
 GGG AAC TGG GAG GGT GCT CTG GAC TAC
 Gly Asn Trp Glu Gly Ala Leu Asp Tyr
 (99-107, CDR 3)

W G Q G T S V T V S S
 TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 (108-118, Fr. #4)

A K T T P P P V Y P L V P G S L
 GCC AAA ACG ACA CCC CCA CCC GTC TAT CCA CTG GTC CCT GGA AGC TTG GG
 Ala Lys Thr Thr Pro Pro Pro Val Tyr Pro Leu Val Pro Gly Ser Leu
 (constant region)

FIG. 2

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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QAYLQQSGAELVRSGASVKMSCKASGYTLT — Framework #1, 1–30
 SYNMH — CDR-1, 31–35
 WVKQTPGQGLEWIG — Framework #2, 36–49
 NIFPGNGDTYYNQKFKG — CDR-2, 50–66
 KASLTADTSSSTAYMQISSLTSEDSAVYFCAR — Framework #3, 67–98
 GNWEGALDY — CDR-3, 99–107
 WGQGTSTTVSS — Framework #4, 108–118

FIG. 3B

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>gb|L41880|MUSIKCC Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.

```

67 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126
127 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 186
187 GATGGAACCTATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 246
247 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 306
307 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGG 366
367 GGGACCAAGCTGGAAATAAAA 387

```

>gb|L48667|MUSX Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA antibody light chain mRNA.

```

1 GANATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
121 GATGGAACCTTTTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 180
181 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTGTCCGTACACGTTCCGGAGGG 300
301 GGGACCAAGCTGGAAATAAAA 321

```

>gb|J00565|MUSIGKAC1 Mouse ig kappa active gene: vk41 v-j region.

```

313 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 372
373 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 432
433 GATGGAACCTATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 492
493 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 552
553 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 612
613 GGCACCAAGCTGGAAATCAAA 633

```

>emb|V00808|MMIGK7 Part of the murine gene for kappa-immunoglobulin leader peptide and variable part (cell line MOPC41).

```

314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373
374 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 433
434 GATGGAACCTATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 493
494 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 553
554 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 613
614 GGCACCAAGCTGGAAATCAAA 634

```

>gb|I03643|I03643 Sequence 4 from patent US 4642334.

```

1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
121 GATGGAACCTATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 180
181 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 300
301 GGCACCAAGCTGGAAATCAAA 321

```

>gb|M59920|MUSIGKAA3 Mouse IG germline chain mRNA V-J region, partial cds.

```

1 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTC 60
61 ACTTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGAC 120
121 GGAACCTATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGG 180
181 TTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAA 240
241 GATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGGAGGC 300
301 ACCAAGCTGGAAATCAAA 318

```

FIG. 4A

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BY	CLASS	SUBCLAS
DRAFTSMAN	WO 97/22699	

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>gb|M36246|MUSIGLAFA Mouse Ig kappa-chain mRNA V region, partial cds. from hybridoma H220-23.

```

1 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCTGGGCAAGT 60
61 CAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACATTAAACGC 120
121 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGG 180
181 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGACTAT 240
241 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCTGGAGGGGGGACCAAGCTGNAAATA 300
301 AAA 303

```

>emb|Z22118|MDIGKVBS M.domesticus IgK variable region.

```

1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACCTTGTCTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 120
121 GATGGAACATTAAACGCCTGATCTACAGCACATCCACTTTAAATTCTGGTGTCCCCAAA 180
181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCTGGAGGG 300
301 GGGACCAAACCTGGAATAAAAA 321

```

>gb|M64168|MUSIGKFT Mouse Ig active kappa-chain mRNA V-region.

```

4 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCTGGGCAAGT 63
64 CAGGACATTGGTAATAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACATTAAACGC 123
124 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGG 183
184 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAATCTGAAGATTTTGTAGTCTAT 243
244 TACTGTCTACAATATGCTAGTTATACGTACACGTTCTGGAGGGGGGACCAAGTTGGAAC 303
304 AAA 306

```

>emb|X02177|MMIGGVJ1 M.musculus mRNA for IgG kappa light chain(partial)
Cloop 1

```

42 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 101
102 CTCACCTTGTCTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 161
162 GATGGAACATTAAACGCCTGATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCCAAA 221
222 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 281
282 GAAGATTTTGCAGACTATTACTGTCTACAATATCTTAGTTATCCGCTCACGTTCTGGTGCT 341
342 GGGACCAAGCTGGAGCTGAAA 362

```

FIG. 4B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLAS
DRAFTSMAN	WO 97/22699	

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>gb|L48668|MUSY Mus musculus (cell line C3H/F2-20) chromosome 12 anti-DNA antibody heavy chain mRNA.

```

1 CAGGCTTATNTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
295 ----- 311
312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

```

>gb|L48680|MUSAL Mus musculus (cell line C3H/F2-3) chromosome 12 anti-DNA antibody heavy chain mRNA.

```

1 CAGGCTTATGTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CGTAGACAGGGCCTGGAATGGATTGGAGCAATTTATCCAGGAAATGGTGATACTTCCTAT 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGATTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGAGA 298
299 GGGGTAACTACGTAGGACATATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 357
358 TCA 360

```

>emb|X64805|MMAIDHCH M.musculus mRNA for anti-Id mAB 114 heavy chain, variable region.

```

1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTAAGGCCTGGGTCCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGGAT 300
301 TACTCCGGTAGTATAGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 354

```

>gb|M17953|MUSIGHXW Mouse Ig rearranged H-chain V-region mRNA VJ1.

```

96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155
156 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215
216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 275
276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
393 ----- 427
428 CTGGGGCACAGGGACCACGGTCACCGTCTCC 458

```

>gb|I05921|I05921 Sequence 37 from patent EP 0274394.

```

96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155
156 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215
216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 275
276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
393 ----- 427
428 CTGGGGCACAGGGACCACGGTCACCGTCTC 457

```

FIG. 5A

APPROVED	O.G. FIG.	
BY	CLASS.	SUBCLASS
DRAFTSMAN	WO 97/22699	

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>emb|Z22117|MDIGGVBC M.domesticus IgG variable region.

```

  2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATAT 61
 62 CCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATGCACTGGGTGAAGCAGAAGC 121
122 CTGGGCAGGGCCTTGAGTGGATTGGAGAGATTTATCCTGGAAGTGGTAATACTTACTACA 181
182 ATGAGAAGTTCAAGGGYAAGGCCTCACTGACTGCAGACAAATCCTCCAGCACAGCCTACA 241
242 TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGACGTTACT 301
302 ----- 314
315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

```

>gb|M15224|MUSIGLAF Mouse IgM H-chain lambda rearranged anti-Dns hybridoma VDJA region of J558 family mRNA.

```

  1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAG 295
296 ----- 314
315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

```

>gb|M15226|MUSIGLAH H-chain lambda rearranged anti-Dns hybridoma VDJA region of J558 family mRNA.

```

  1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
295 ----- 317
318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

```

>gb|M15225|MUSIGLAG H-chain lambda rearranged anti-Dns hybridoma VDJA region of J558 family mRNA.

```

  1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
295 ----- 311
312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

```

>gb|M20835|MUSIGKCLP Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody.

```

106 CAGGTCCAACCTGCAGCAGCCTGGTGCTGAGCTTGTGAAGCCTGGGGCCTCAGTGAAGCTG 165
166 TCCTGCAAGGCTTCTGGCTACACTTTACCAGCTACTGGATAAACTGGGTGAAGCAGAGG 225
226 CCTGGACAAGGCCTTGAGTGGATTGGAAATATTTATCCTGGTAGTAGTACTAAGTAC 285
286 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACATCCTCCAGCACAGCCTAC 345
346 ATGCAGCTCAGCAGCCTGACATCTGACGACTCTGCGGTCTATTATTGTGCAAGACG 401
402 ----- 416
417 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 462

```

FIG. 5B

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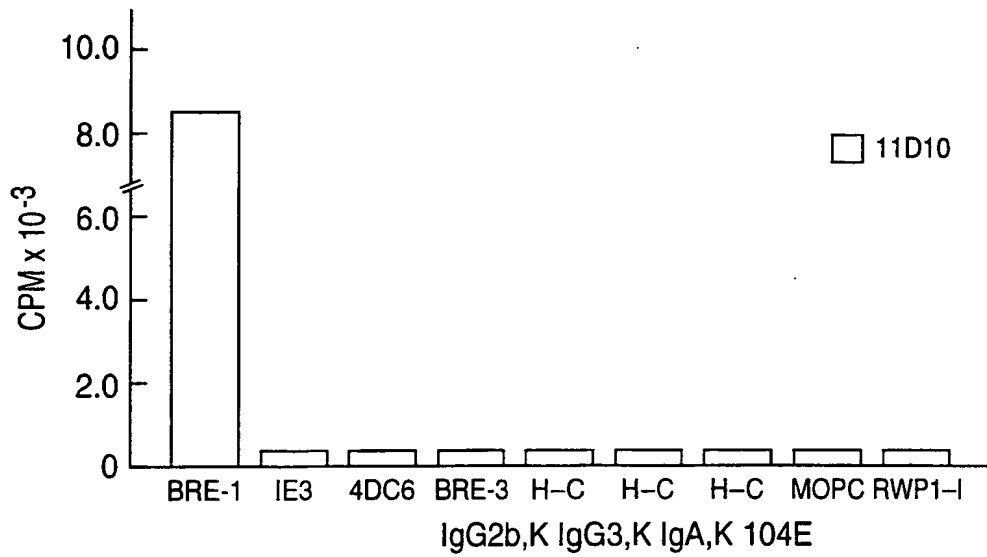


FIG. 6

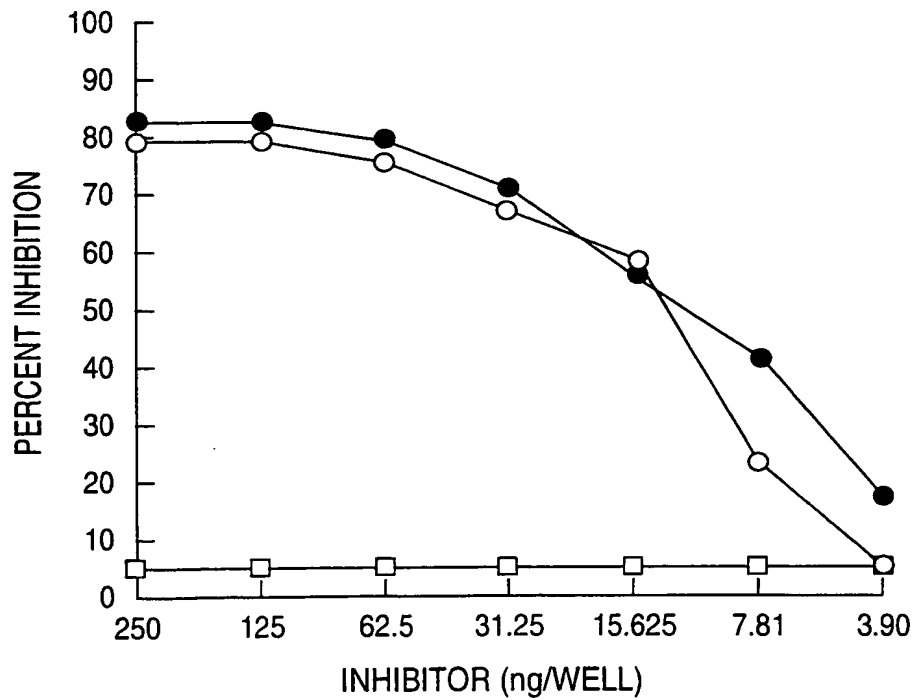


FIG. 7

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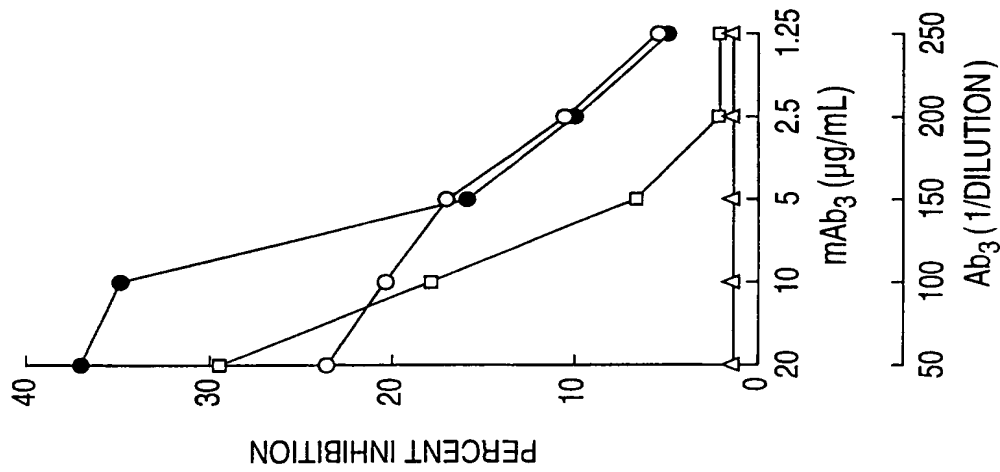


FIG. 9

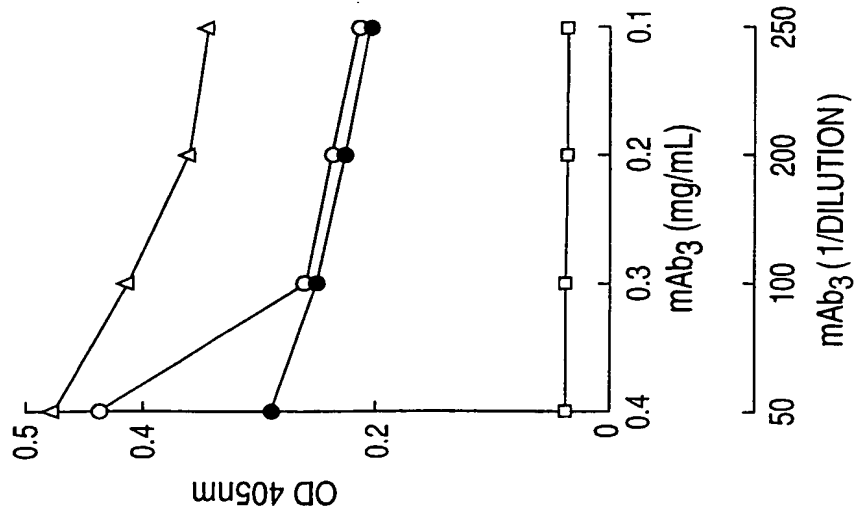


FIG. 8

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 97/22,699	

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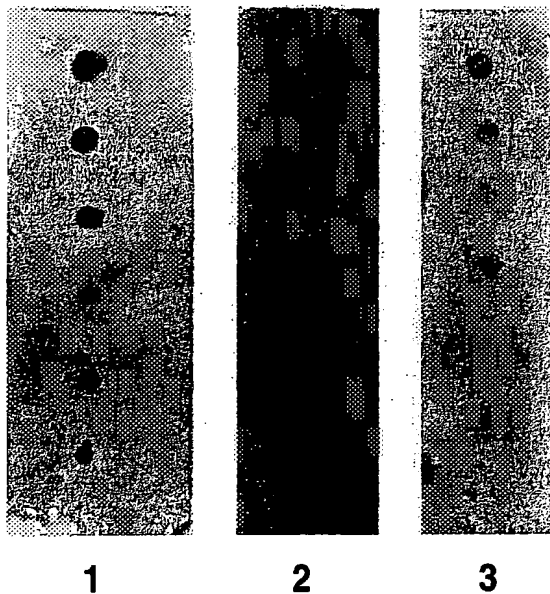


FIG. 10

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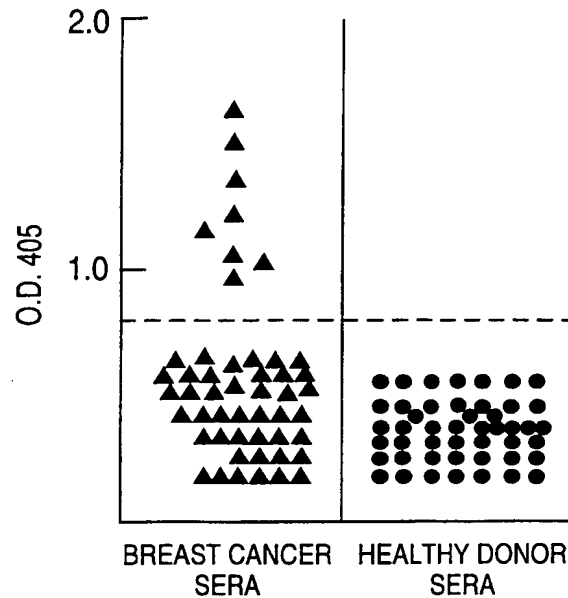


FIG. 11

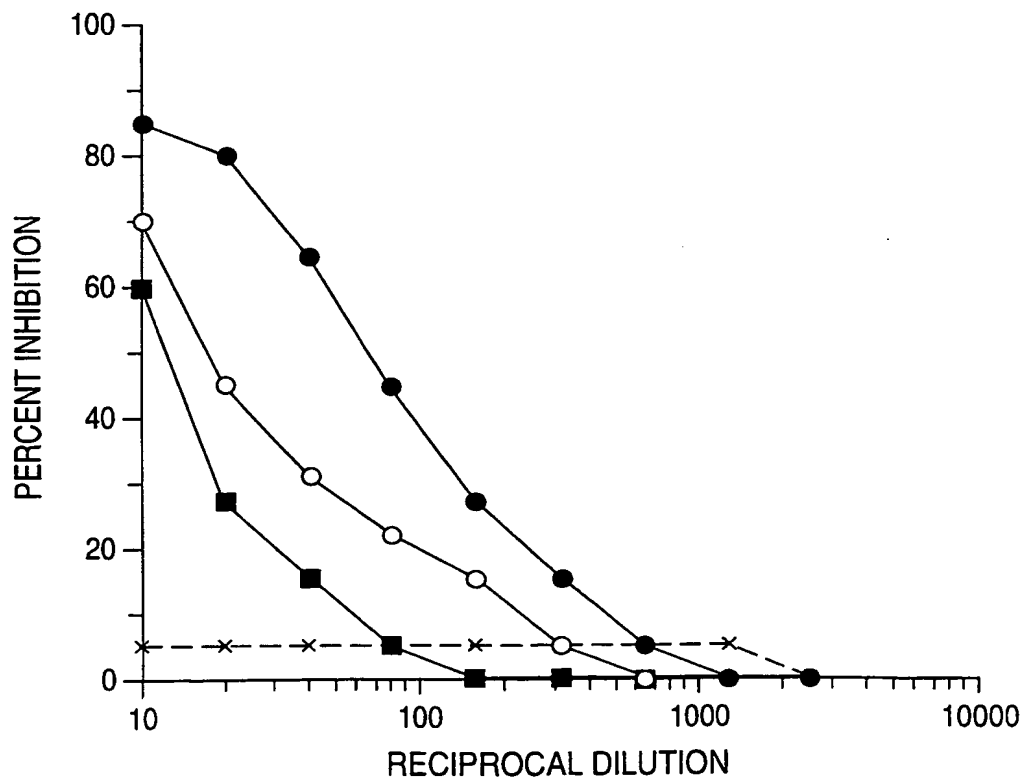


FIG. 12

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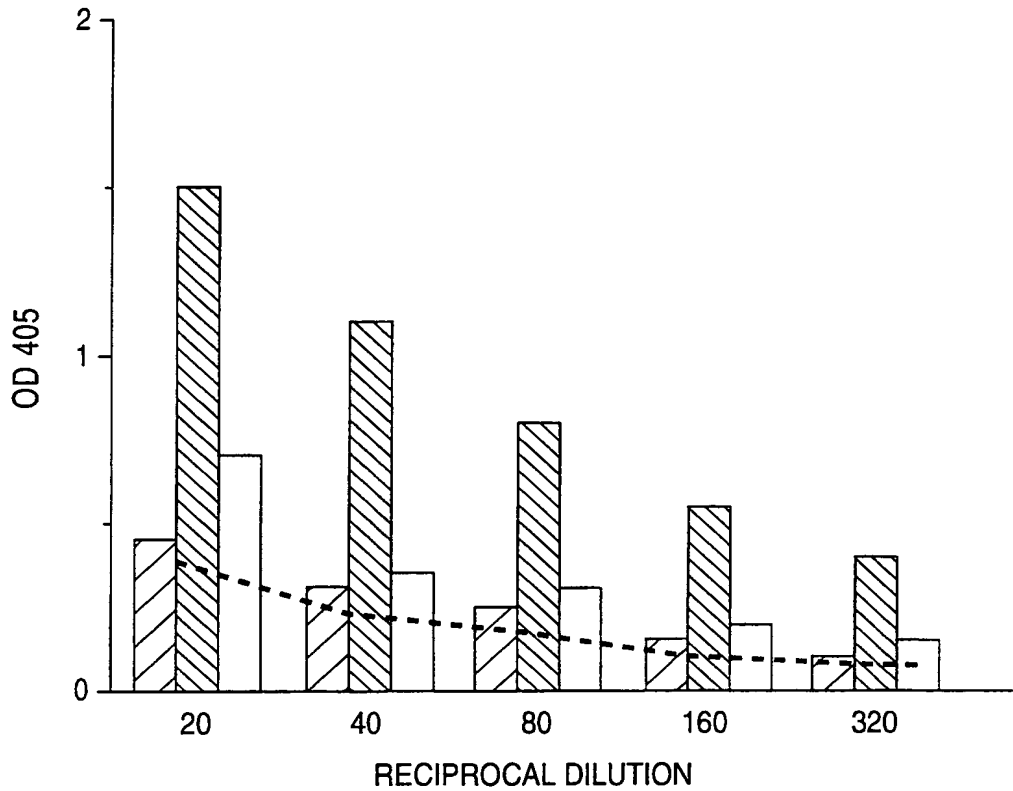


FIG. 13

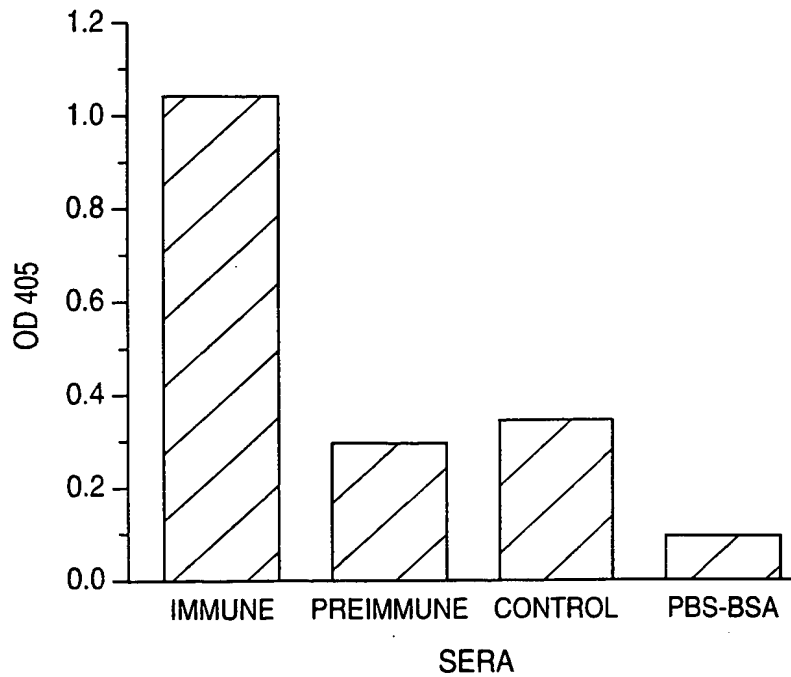


FIG. 14

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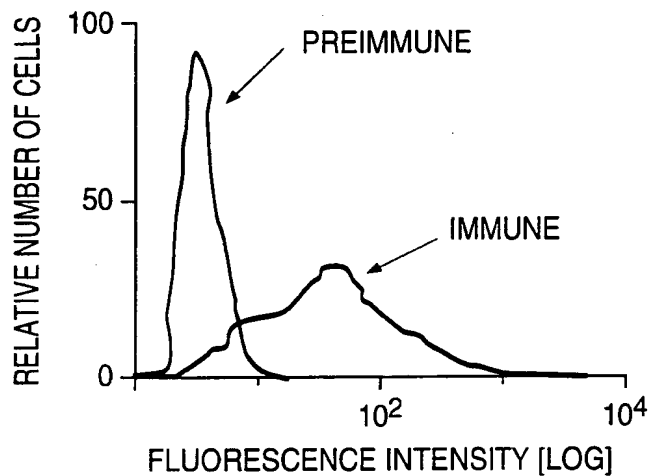


FIG. 15A

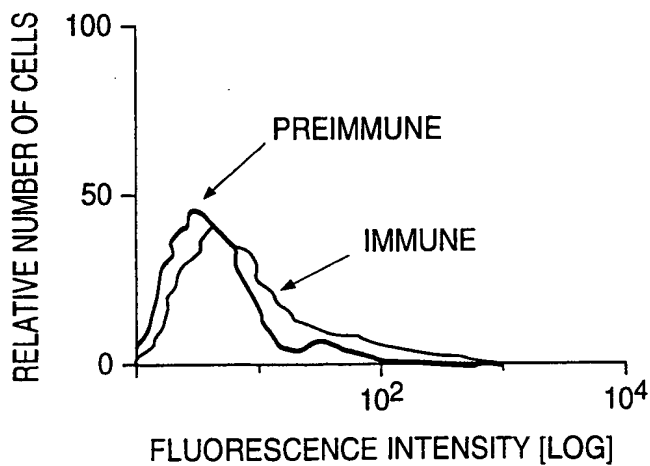


FIG. 15B

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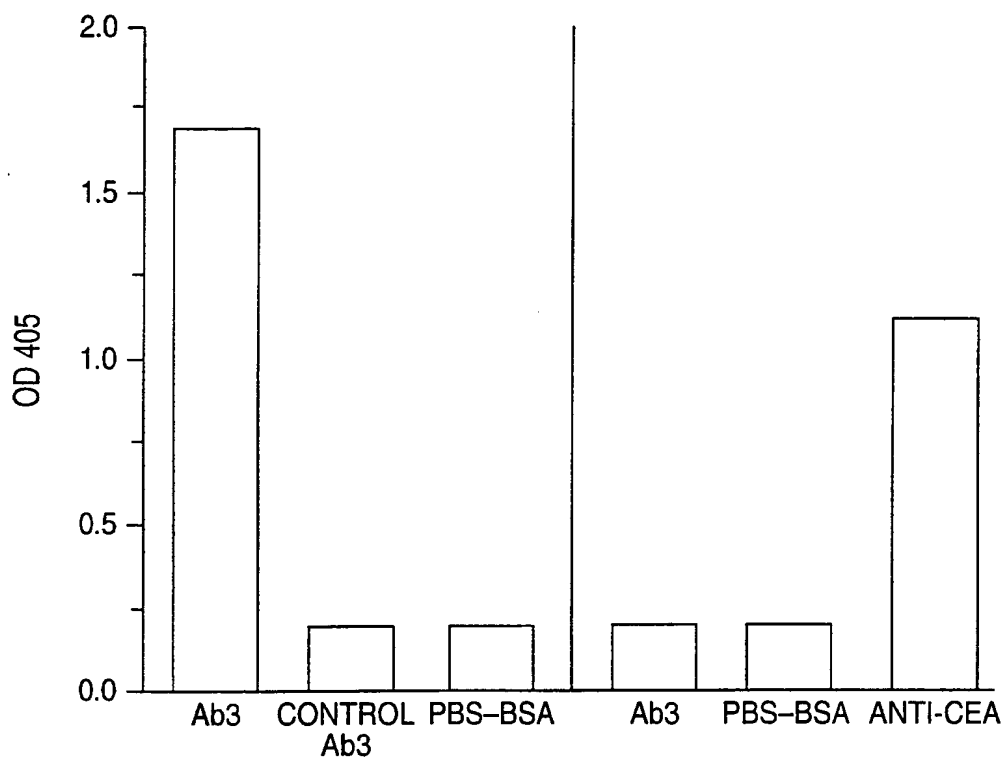


FIG. 16

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLAS
DRAFTSMAN WO 97/22699		

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1 2 3 4

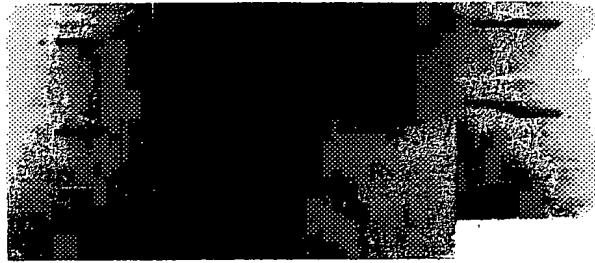


FIG. 17

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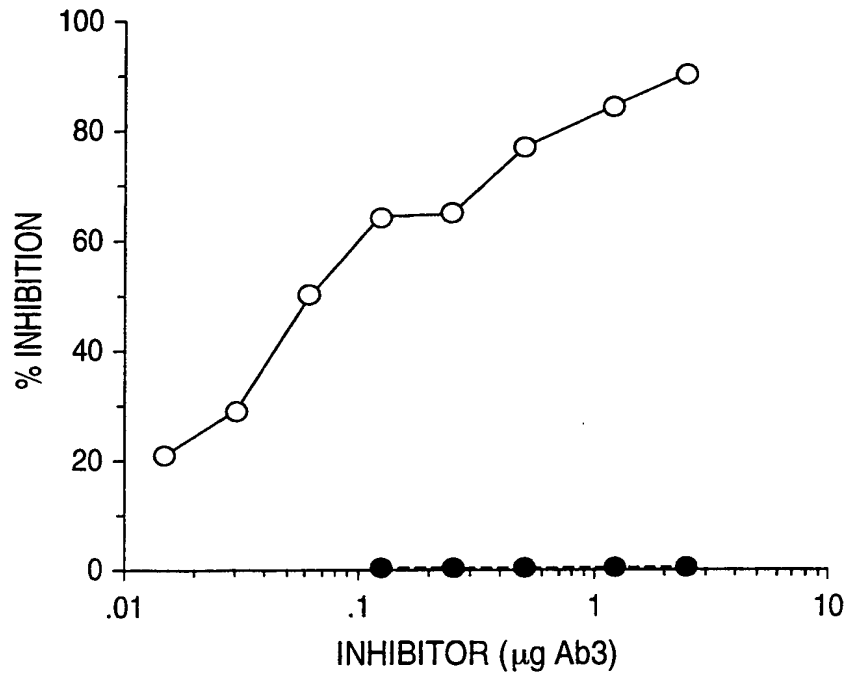


FIG. 18

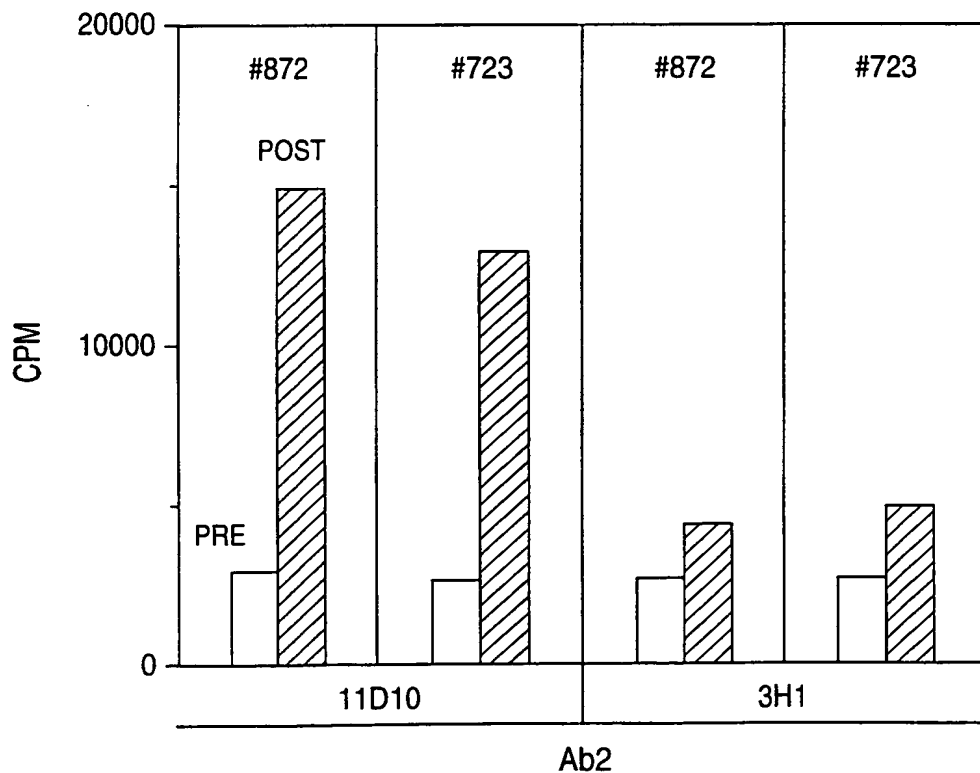


FIG. 19

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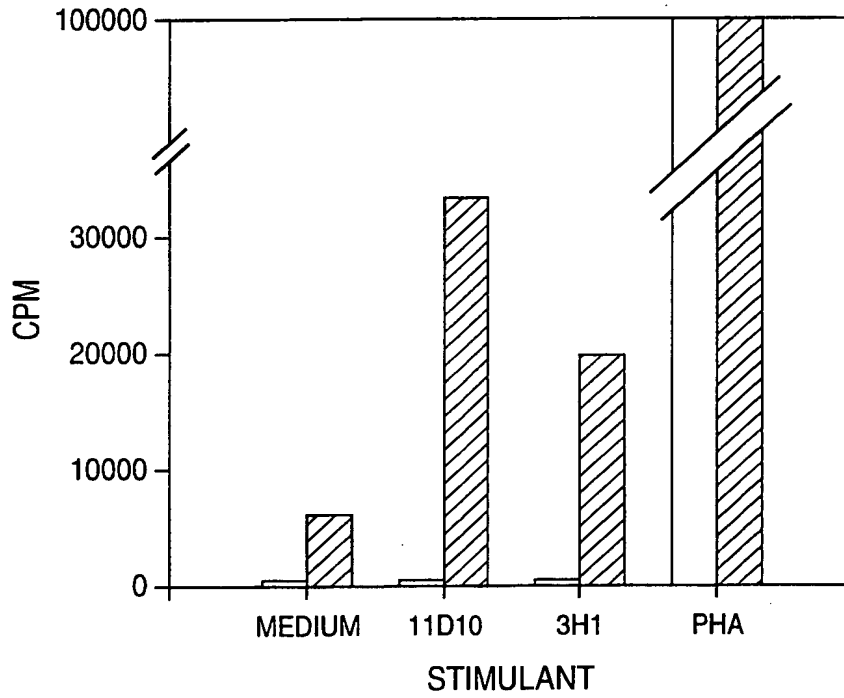


FIG. 22

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 91/22699	

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Q G L E W I G N I F P G N G D T Y Y N O

: : : : | |

R E S P

G S T A P P A H G V T S A P D T R P A P

: | : | : |

D G T I K R L I Y A T S S L G S G V P L

P S E R P

P A P R T D P A S T V G H A P P A T S G P A P

: | : | : : : | | : :

H T L Q Q E P D G T I K R L I Y A T S S L G S

: | : : : |

A Y Y C L O Y A S S P Y T F G G G T K L E I K

V_H (NEAR CDR 2)

HMFG REPEAT (DIRECT)

V_L (NEAR CDR 2)

HMFG REPEAT (REV.)

V_L (NEAR CDR 2)

V_L (NEAR CDR 2)

FIG. 23

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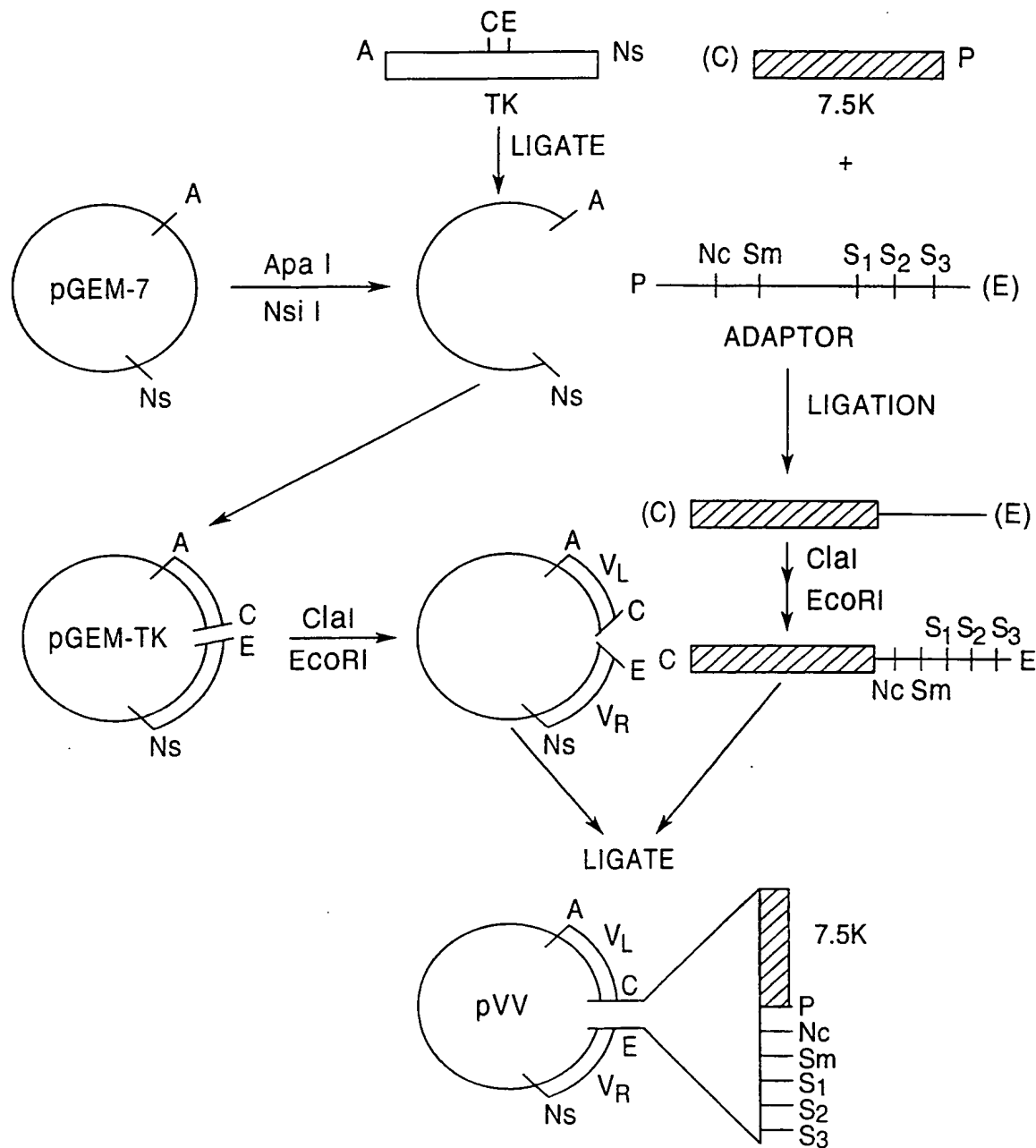


FIG. 24

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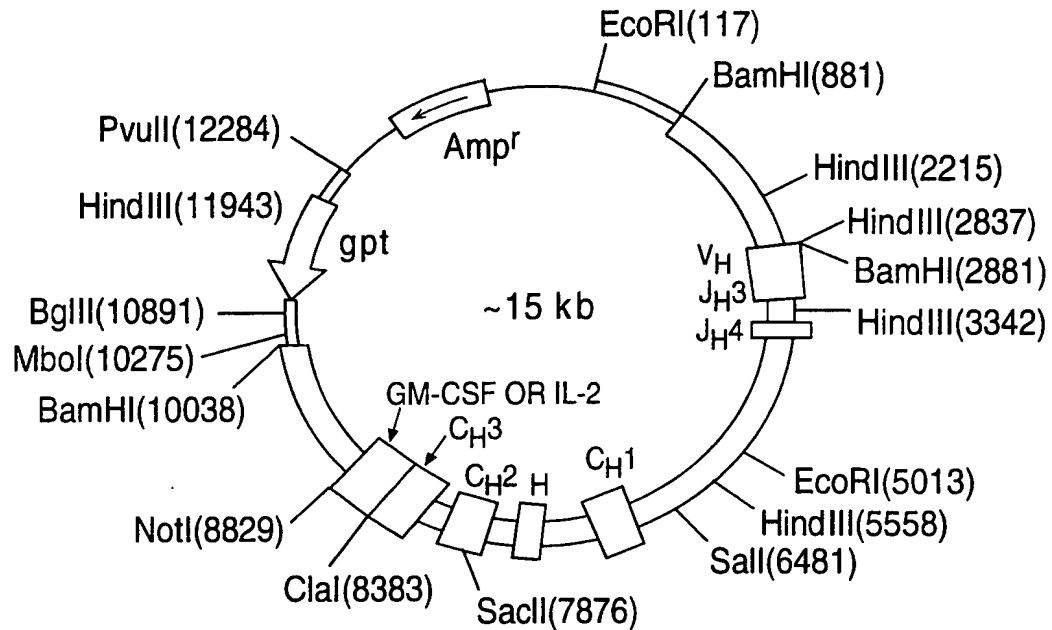


FIG. 25A

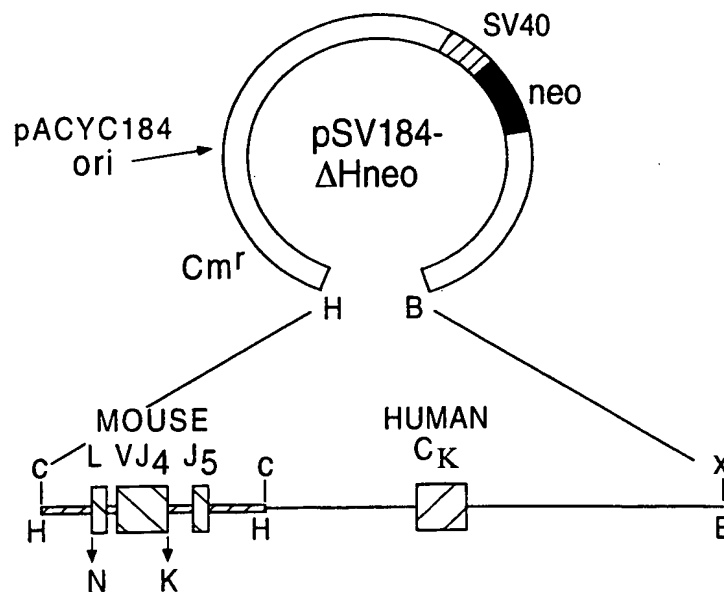


FIG. 25B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 97	22699

08/836455

PCT/US96/20757

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11D10: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60

1	23E.....SS.NW.....D.....	82
2	23E.....SS.NW.....D.....	82
3	23E.....SS.NW.....D.....	82
4	23E.....P.....SS.NW.....D.....	82
5	1E.....SS.NW.....D.....	60
6	1E.....SS.NW.....D.....	59
7	1E.....RS.NW.....D.....	60
8	1E.....E.SGY.SW...K.....S..T.N.....	60
9	1E.....SS.NW.....D.....	54
10	1E.....E.SGY.SW...K.....A.T.D.....	60
11	1	X.....E.....NS.NW.....D.....	55
12	1E.....A.....E..GY.SW...K.....A.T.D.....	60
13	14E.....E.SGY.SW...K.....A.T.D.....	73
14	1	EL.....E.....E.SGY.SW...K.....A.T.D.....	60
15	2	ELVL.....E.....E.NGY.GW...K.....A.T.H.....	61

11D10: 61 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIK 107

1	83D.....	129
2	83D.....W.....	129
3	83D.....W.....	129
4	83D.....W.....	129
5	61D.....W.....	106
6	60D.....W.....	106
7	61D.....T..W.....	106
8	61AD.....	107
9	55D.....X.....	107
10	60AD.....	106
11	56V.....YT.....L.....	102
12	61	..G.....AD.....Y.W.....	106
13	74AD.....L.Y.L...A....L.....	120
14	61AD.....Y.L...A....L.....	107
15	62AD.....Y.R.....	108

FIG. 26A

SUBSTITUTE SHEET (RULE 26)

0836455-050997

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 97/22699	

08/836455

PCT/US96/20757

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11D10: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60

1	1P.S.....F.....R.....A.Y.....S.	60
2	20P.....F.....R.....A.Y.....S.	79
3	1	EVQ.....P...KP.....I.....F.D.Y.....K.....E.Y..S.N...	60
4	1	.IQ.....P...P.....I.....F.D.YI.....R..E.....W.Y..S.N.K.	60
5	1	.VQ.....P...KP.....L.....F.D.TI.....S.....W.Y..S.N.K.	60
6	1	.VQ...E.....KP.....L.....F..W.....R.....K.N.S..R.N.	60
7	20	.VQ.....AKP.....F.A.W.....R.....Y.N.NT.Y.E.	79
8	1	EVQ.....KP.....L.....F..W.....R.....E.D.SDSY...	60
9	1	.VQ...E...A.P.....F.R.W.....R...A....A.Y...S..N.	60
10	1	.VQ.....P.T...I.....F.N.WLG....R..H.....D.Y..G.Y.N.	60
11	20	.VQ.....AKP.....F..R.....R.....Y.N.ST.Y.E.	79
12	1	.VQ.....AKP.....F..W.....R.....Y.N.ST.Y.E.	60
13	1	.IQ.....P...P.....I.....F.D.YI.....R..E.....W.Y..S.N.K.	60
14	1	.VQ.....P.T.....A...F.N.WIG....R..H.....D.Y..G.Y.N.	60
15	1	EVQ.....TV.A.P.....F..W.....R.....A.Y...S..R.	60

11D10: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG=NWEG=ALDYWGQGTSTVTVSS 118

1	61T..V.K.....L.....=DYS.=SI.....TL....	118
2	80T..V.K.....L.....xxxxxxxxxx=xx.V..T..T....	140
3	61	.E.....K.....L.....xxxxxxxxx=.M.....	120
4	61	.E.....T..V.....L.....=xxx=.M.....	117
5	61	.D.....TM...K.....L.....=VAR.S=.M.....	119
6	61	.E...S..T..V.K.....L.....Y...xxxxxxxxx.....T....	123
7	80	..N..D..T...K.....L.....Y.T.xxx.Y...=.M.....	139
8	61T..V.K.....F.....Y...xxxxxxxxx=xM.....	120
9	61K...V..A....EL..A....Y...S=R.YR.=SM.....	119
10	61	.E.....T.....L.....P=HYY.=SG.....TL....	118
11	80D..T...K.....L...F.....Y...=x.=VF.....TL....	135
12	61D..T...K.....L.....L.Y...W=VYYY=.M.....	118
13	61	.E.....T..V.....L.....=xxx=.M.....	117
14	61	.E.....T.....L.....I.Y...P=F.YFY=.M.....C....	118
15	61K...V..A....EL...N....Y.T...=GLFT=.M.....	115

FIG. 26B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 97/22699	

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Light Chain

VL consensus: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDGVPK 60
 11D10: 1Q.....IN.HT.....G..... 60

HMFG fragments: GSIAPPAHRVTSAPESRPPP
 pprsepastvrhappatsg

VL consensus: 61 RFSGSRSGSDYSLTISSLESQDFVDYYCLQYASSPYTFGGGKLEIK 107
 11D10: 61A..... 107

HMFG fragments: pprsepastvrhappatsg

Heavy Chain

VH consensus: 1 QVQLQQSGAELVRPGASVKMSCKASGYTFTSYWMHWKQRPQGQLEWIGAIYPGNGDTNY 60
 11D10: 1 .AY.....S.....L...N.....T.....N.F.....Y. 60

HMFG fragments: APDTRPPP

VH consensus: 61 NQKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARGxxxGAMDYWGQGTSTVTVSS 118
 11D10: 61S.....I.....NWE..L..... 118

FIG. 26C

08/836455-050997

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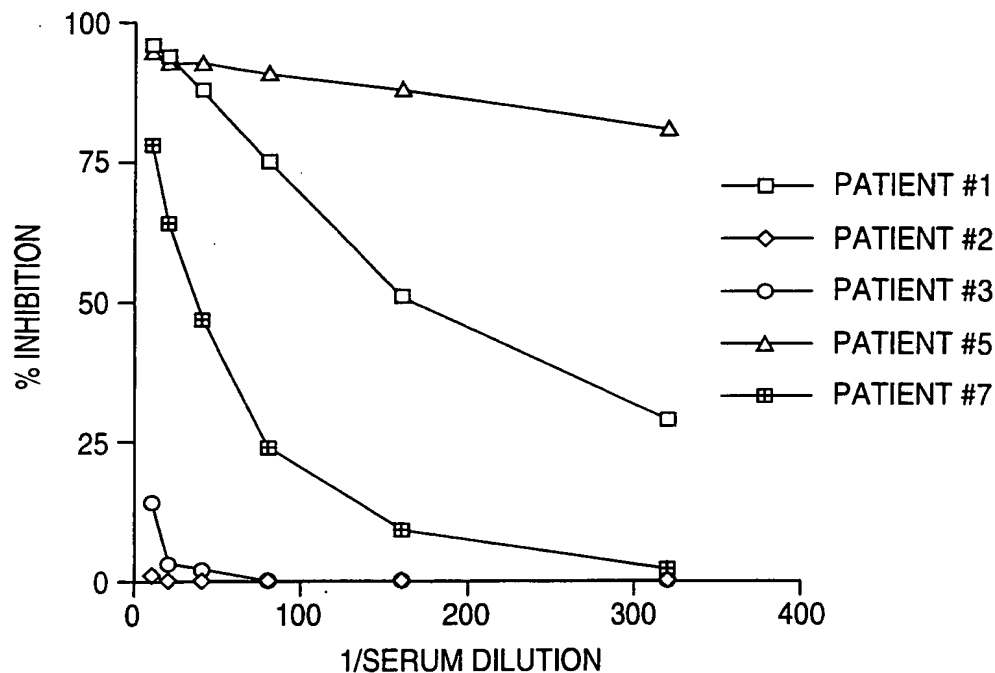


FIG. 27A

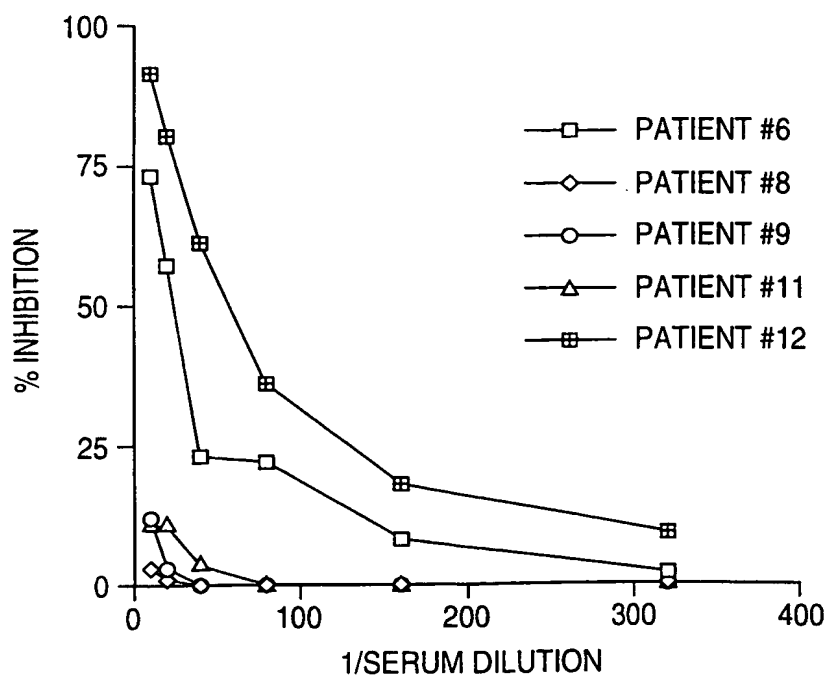


FIG. 27B

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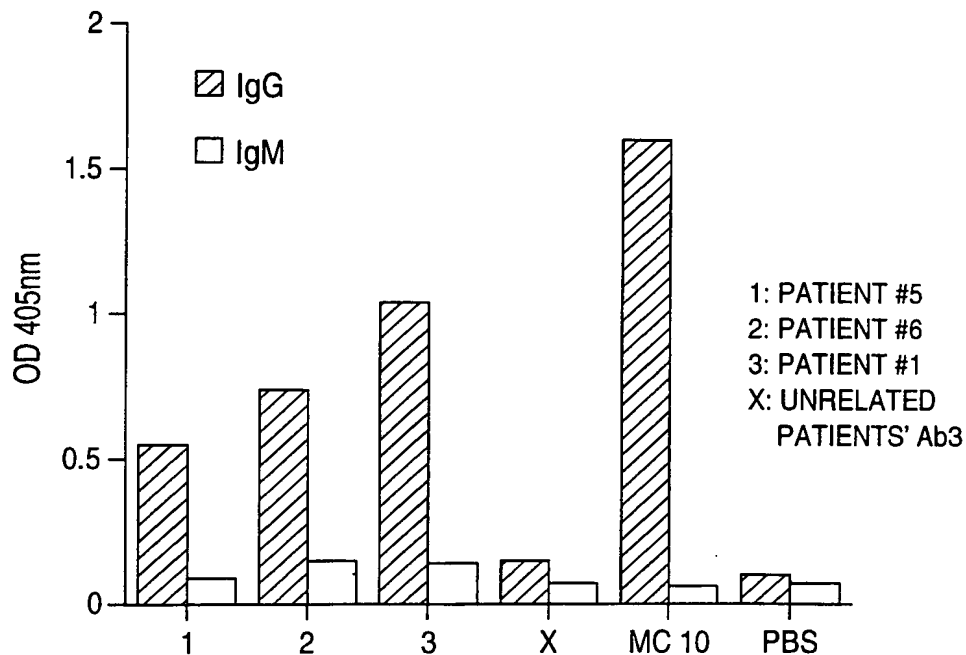


FIG. 28

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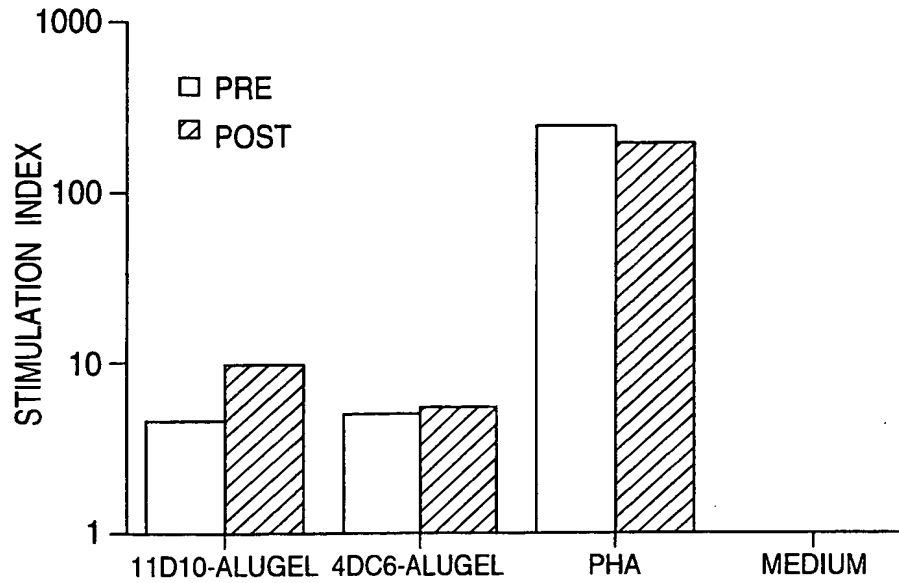


FIG. 29A

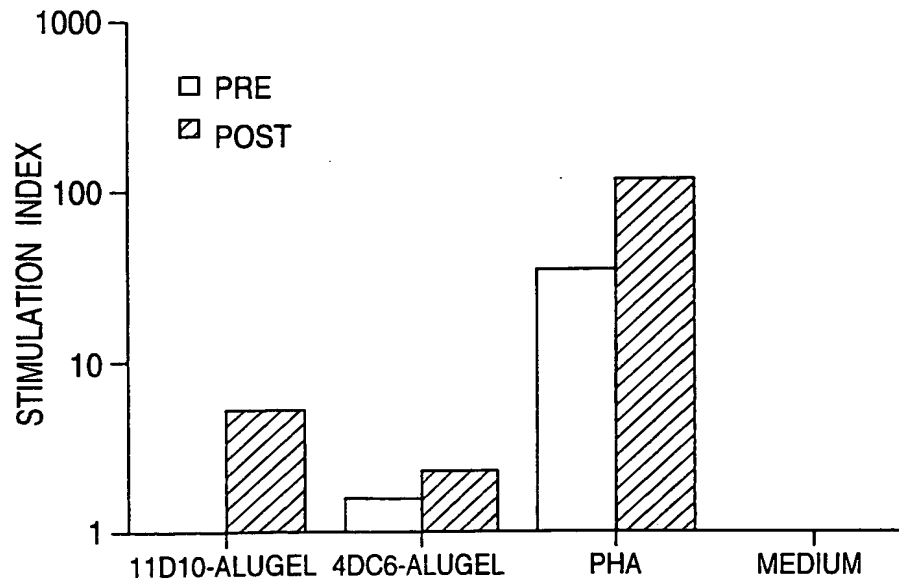


FIG. 29B